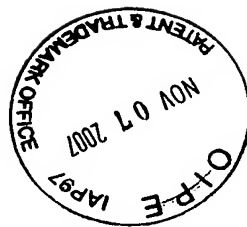


feline (from cDNA) YEIAPVFVLMEQITLKKMREIVGWSSKDGDFSPGGAINMYSIMAAARYKFFPEVKTKG

rat (from peptide) YEIAPVFVLLEYV-----REIIGWPGGS-DGIFSPGGAIN-YAMLIARYKMFPEVKEKG

Figure 1



```

GGCGTGC GGGT C GAGCC G AAGC AGCTT G CCGC G CAGCC ACTCG GAGG CGCAG CGGCCA
10          30          50
      M A S P G S G F W S F G S E D G
GACTAGC AGAACC CATGG CATCTCC GGGCTCTGG CTTT TGGT CCTTC G GATCTG AAGATG
70          90          110
      S G D P E N P G T A R A W C Q V A Q K F
GCTCTGG GATCCT GAGAA CCGGGA ACAGC GAGAG CCTGT GTGCC AGTG GCGCC CAAAAGT
130          150          170
      T G G I G N K L C A L L Y G D S E K P A
TCACGGG CGCATC GGAACA AGCTAT GCGCTCT GCTCT ACGGAG ACTCTG AGAAG CCGAG
190          210          230
      E S G G S V T S R A A T R K V A C T C D
CAGAGAG CGGCGG AGCGTG ACCTC GCGGG CGGCC ACTCG GAAGT CGCTG CACCTGTG
250          270          290
      Q K P C S C P K G D V N Y A L L H A T D
ACCAAAA ACCCTG CAGCTG CCCC AAGGAG ATGTCA ATTAT GCACTT CTCCAC GCAACAG
310          330          350
      L L P A C E G E R P T L A F L Q D V M N
ACCTGCT GCCAGC CTGTGA AGGAA AGCCCC ACTCTC GCAATT TCTGCA AGATGT AATGA
370          390          410
      I L L Q Y V V K S F D R S T K V I D F H
ACATTTT GCTTCA GTGGTG AAAAGT TTTGAT AGATCA ACTAA AGTGAT TATTCC
430          450          470
      Y P N E L L Q E Y N W E L A D Q P Q N L
ATTACCCC AATGAG CTTCTT CAAGAG TATAAT TGGGA ATTGGC AGACCA CCGCAA ATC
490          510          530
      E E I L T H C Q T T L K Y A I K T G H P

```

Figure 2A

TGGAGGAAATTTTGACGCACTGCCAAACAACCTCTAAATATGCGATTAAACAGGGCATC
 550 570 590
 R Y F N Q L S T G L D M V G L A A D W L
 CCCGATATTTTAATCAGCTGTCTACCGGATTGGATATGGTTGGATTAGCAGCATTTGGT
 610 630 650
 T S T A N T N M F T Y E I A P V F V L L
 TGACATCAACAGCAACACGAACATGTTTACCTATGAGATCGCCCTGTATTGTACTAC
 670 690 710
 E Y V T L K K M R E I I G W P G G S G D
 TGGAATATGTGACACTAAAGAAAATGAGGGAATCATTTGGCTGGCCAGGAGGCTCTTGGCG
 730 750 770
 G I F S P G G A I S N M Y A M L I A R Y
 ATGGAATCTTTTCTCTGGTGGTGCCATCTCCAACATGTACGCCATGCTCATTTGCCCGCT
 790 810 830
 K M F P E V K E K G M A A V P R L I A F
 ATAAGATGTTTCCAGAAGTCAAGGAAAAGGGGATGGCGGGTGCCAGGCTCATCGCAT
 850 870 890
 T S E H S H F S L K K G A A A L G I G T
 TCACGTCAGAGCATAGTCACTTTTCTCTCAAGAAGGAGCTGCAGCCTTGGGGATCGGAA
 910 930 950
 D S V I L I K C D E R G K M I P S D L E
 CAGACAGCGTGATTCTGATTAAATGTGATGAGAGAGGGAATAATGATCCCCTGTACCTTG
 970 990 1010
 R R I L E V K Q K G F V P F L V S A T A
 AAAGAAGAATCCTTGAAGTCAAAACAGAAAGGATTTGTTCCCTTTCCCTGGTGAGTGCCACAG
 1030 1050 1070
 G T T V Y G A F D P L L A V A D I C K K

Figure 2B

CTGGAACCACTGTGTACGGGGCTTTTGGATCCTCTCTTGGCTGTAGCTGACATCTGCAAAA
 1090 1110 1130
 Y K I W M H V D A A W G G L L M S R K
 AATAAGATCTGGATGTCATGTGGATGCTGCTTGGGGTGGAGGGTTACTGATGTCTCGGA
 1150 1170 1190
 H K W K L N G V E R A N S V T W N P H K
 AACACAAGTGGAAGCTGAACGGTGTGGAGAGGGCCAACTCTGTGACATGGAATCCCCACA
 1210 1230 1250
 M M G V P L Q C S A L L V R E E G L M Q
 AGATGATGGGTGTCCTTGGCAATGTTCCGGCTCTCCTGGTCAGAGAGGGACTGATGC
 1270 1290 1310
 S C N Q M H A S Y L F Q Q D K H Y D L S
 AGAGCTGCAACCAGATGCATGCTTCCCTACCTCTTTTCAGCAAGATAAGCACTATGACCTGT
 1330 1350 1370
 Y D T G D K A L Q C G R H V D V F K L W
 CCTATGACACGGGAGACAAGGCCTTGCAGTGTGGACGCCACGTCGATGCTTTAAATTAT
 1390 1410 1430
 L M W R A K G T T G F E A H I D K C L E
 GGCTCATGTGGAGAGCAAAGGGACTACTGGATTTGAAGCTCACATTGATAAGTGTTCG
 1450 1470 1490
 L A E Y L Y N I I K N R E G Y E M V F D
 AGCTGGCAGAGTATTATACAATATCATTAATAAACCGAGAAGGATATGAAATGGTGTTCG
 1510 1530 1550
 G K P Q H T N V C F W F V P S L R V L
 ATGGGAAGCCTCAGCACACAAATGTCTGCTTCTGTGTTTGTACCTCCTAGTTTGGGAGTTC
 1570 1590 1610
 E D N E E R M S R L S K V A P V I K A R

Figure 2C

TGGAAGACAAATGAAGAGAGAATGAGCCGCCCTCTCAAAGGTGGCGCCAGTGATTAAAGCCA	1630	1650	1670
M M E Y G T T M V S Y Q P L G D K V N F			
GAATGATGGAGTATGGGACCACAAATGGTCAGCTACCAACCCTTAGGAGATAAGGTCAACT	1690	1710	1730
F R M V I S N P A A T H Q D I D F L I E			
TCTTCCGCATGGTCATCTCAAACCCTGCAGCAACTCACCAAGACATTGACTTCCTCATTTG	1750	1770	1790
E I E R L G Q D L *			α
AAGAAATCGAACGCCCTGGGACAAAGATTTGTAAATCACTTTGTCTCACCAAACTTTTCAGTTCT	1810	1830	1850
CTAGGTAGACAGCTAAGTTGTCAAAACTGTGTAAATGTATTTGTAGTTTGTTCAGAGT	1870	1890	1910
AATTCATTTTCTATATCGTGGTGTCAACAGTAGAGTCCAGTTTAAAA	1930	1950	

Figure 2D

AGCTCGCCCGCAGCTCGCACTCGCAGGCGACCTGCTCCAGTCTCCAAAGCCGATGGCATC
10 30 50
P G S G F W S F G S E D G S G D S E N P
TCCGGGCTCTGGCTTTTGGTCTTTTCGGGTCCGGAAGATGGCTCTGGGATTCGAGAATCC
70 90 110
G T A R A W C Q V A Q K F T G G I G N K
CGGCACAGCGGAGCCCTGGTGCCAAAGTGGCTCAGAAGTTCACGGGCGGCATCGGAACAA
130 150 170
L C A L L Y G D A E K P A E S G G S Q P
ACTGTGCGCCCTGCTCTACGGAGACGCCGAGAACGCCGCGGAGAGCGCGGAGCCAAACC
190 210 230
P R A A A R K A A C A C D Q K P C S C S
CCCGGGCGCCGCCGGAAGCGCGCTGCGCCTGCGACACAGAACCCCTGCAGCTGCTC
250 270 290
K V D V N Y A F L H A T D L L P A C D G
CAAAGTGATGTCAACTACGCGTTTCTCCATGCAACAGACCTGCTGCCGCGTGTGATGG
310 330 350
E R P T L A F L Q D V M N I L L Q Y V V
AGAAAGGCCCACTTTGGCGTTTCTGCAAGATGTTATGAACATTTTACTTCAGTATGTGGT
370 390 410
K S F D R S T K V I D F H Y P N E L L Q
GAAAAGTTTCGATAGATCAACCAAGTGATTGATTTCATTATCCTAATGAGCTTCTCCA
430 450 470
E Y N W E L A D Q P Q N L E E I L M H C
AGAATATAATTGGGAATTGGCAGACCAACCAACAAAATTTGGAGGAAAATTTTGATGCATTG

Figure 3A

490 510 530
 Q T L K Y A I K T G H P R Y F N Q L S
 CCAACAACCTCTAAAATATGCAATTAAACAGGCGATCCTAGATACTTCAATCAACTTTC
 550 570 590
 T G L D M V G L A A D W L T S T A N T N
 TACTGGTTTGGATATGGTTGGATTAGCAGCAGACTGGCTGACATCAACAGCAATACTAA
 610 630 650
 M F T Y E I A P V F V L L E Y V T L K K
 CATGTTCAACCTATGAAATTGCTCCAGTATTTGTGCTTTTGGAAATATGTCACACTAAAGAA
 670 690 710
 M R E I I G W P G G S G D G I F S P G G
 AATGAGAGAAATCATTTGGCTGGCCAGGGGCTCTGGCGATGGGATATTTTCTCCCGGTGG
 730 750 770
 A I S N M Y A M M I A R F K M F P E V K
 CGCCATATCTAACATGTATGCCATGATGATCGCAGCTTTAAGATGTTCCAGAAAGTCAA
 790 810 830
 E K G M A A L P R L I A F T S E H S H F
 GGAGAAAGGAATGGCTGCTCTTCCAGGCTCATTTGCCTTCACGTCTGAACATAGTCATTT
 850 870 890
 S L K K G A A A L G I G T D S V I L I K
 TTCTCTCAAGAAGGAGCTGCAGCCTTAGGGATTGGAACAGACAGCGTGATTCTGATTAA
 910 930 950
 C D E R G K M I P S D L E R R I L E A K
 ATGTGATGAGAGAGGGAATGATTCCATCTGATCTTGAAGAAGGATTCTTGAAGCCAA
 970 990 1010
 Q K G F V P F L V S A T A G T T V Y G A

Figure 3B

ACAGAAAGGGTTTGTTCCTTTCCCTGAGTGCCACAGCTGGAACCAACCGTGACGGAGC
 1030 1050 1070
 F D P L L A V A D I C K K Y K I W M H V
 ATTTGACCCCTCTTAGCTGCTGCTGACATTGTGCAAAAAGTATAAGATCTGGATGCATGT
 1090 1110 1130
 D A A W G G G L L M S R K H K W K L S G
 GGATGCAGCTTGGGTGGGGATTACTGATGTCCCGAAACACAAGTGGAACCTGAGTGG
 1150 1170 1190
 V E R A N S V T W N P H K M M G V P L Q
 CGTGGAGAGGGCCAACTCTGTGACGTGGAATCCACACAAGATGATGGAGTCCCTTTGCA
 1210 1230 1250
 C S A L L V R E E G L M Q N C N Q M H A
 GTGCTCTGCTCTCCTGTTAGAGAAGAGGGATTGATGCAGAATTGCAACCAAAATGCATGC
 1270 1290 1310
 S Y L F Q Q D K H Y D L S Y D T G D K A
 CTCCTACCTCTTTCAGCAAGATAAACATTATGACCTGTCTCTATGACACTGGAGACAAGGC
 1330 1350 1370
 L Q C G R H V D V F K L W L M W R A K G
 CTTACAGTGGGACGCCACGTTGATGTTTTTAAACTATGGCTGATGTGGAGGGCAAAGGG
 1390 1410 1430
 T T G F E A H V D K C L E L A E Y L Y N
 GACTACCGGTTTGAAGCGCATGTTGATAAAATGTTTGGAGTTGGCAGAGTATTTATACAA
 1450 1470 1490
 I I K N R E G Y E M V F D G K P Q H T N
 CATCATAAAAAACCGAAGGATATGAGATGTTGTTTGTGATGGGAAGCCTCAGCACACAAA
 1510 1530 1550

Figure 3C

V C F W Y I P P S L R T L E D N E E R M
TGTCTGCTTCTGTACATTCTCCAAGCTTGCGTACTCTGGAAGACAATGAAGAGAGAAT
1570 1590 1610
S R L S K V A P V I K A R M M E Y G T T
GAGTCGCCCTCTCGAAGGTGGCTCCAGTGATTAAAGCCAGAATGATGGAGTATGGAACCCAC
1630 1650 1670
M V S Y Q P L G D K V N F F R M V I S N
AATGGTCAGCTACCAACCCCTTGGGAGACAAGGTCAATTTCTTCCGCATGGTCATCTCAAA
1690 1710 1730
P A A T H Q D I D F L I E E I E R L G Q
CCCAGCGGCAACTCACCAAGACATTGACTTCCCTGATTGAAGAAATAGAACGCCCTTGGACA
1750 1770 1790
D L *
AGATTTATAATAACCTTGCTCACCAAGCTGTTCACACTTCTCTAGGTAGACAAATTAAGTTG
1810 1830 1850
TCACAAACTGTGTGAATGTATTTGTAGTTTGTTCCAAAGTAAATCTATTTCTATATTGTG
1870 1890 1910
GTGTCAAAGTAGAGTTTAAAAATTAAACAAAAAAGACATTGCTCCTTTTAAAAAGTCCTTT
1930 1950 1970
CTTAAGTTTAGAATACCTCTCTAAGAATTCGTGACAAAAGGCTATGTTCTAATCAATAAG
1990 2010 2030
GAAAAGCTTAAAAATTGTTATAAATACTTCCCTTACTTTTAATATAGTGTGCAAGCAAAC
2050 2070 2090

Figure 3D

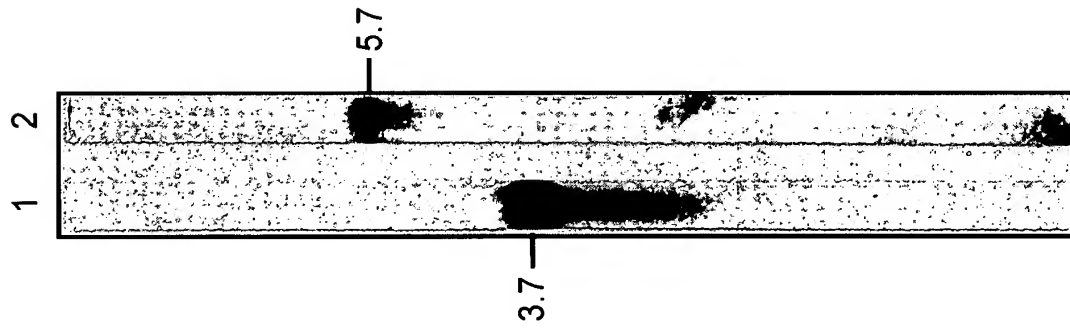


Figure 5

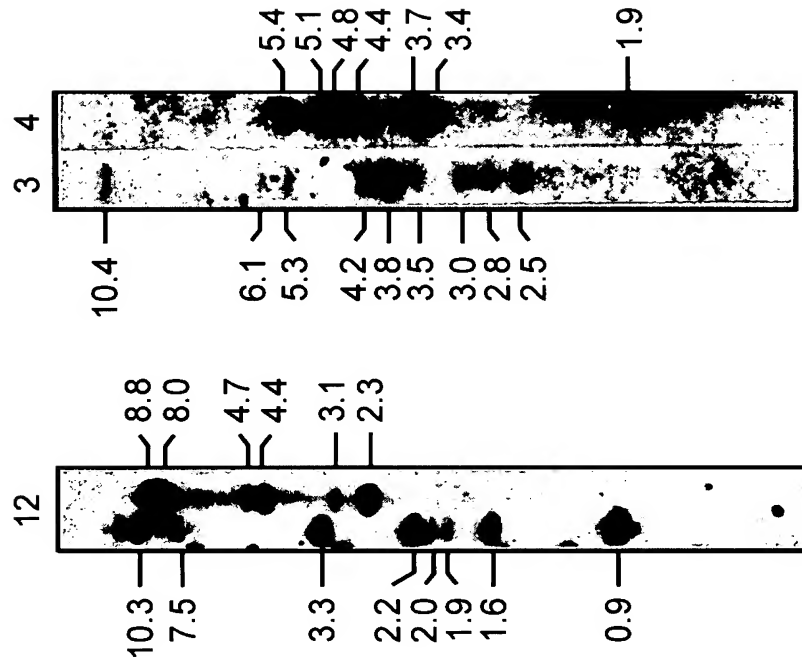


Figure 6

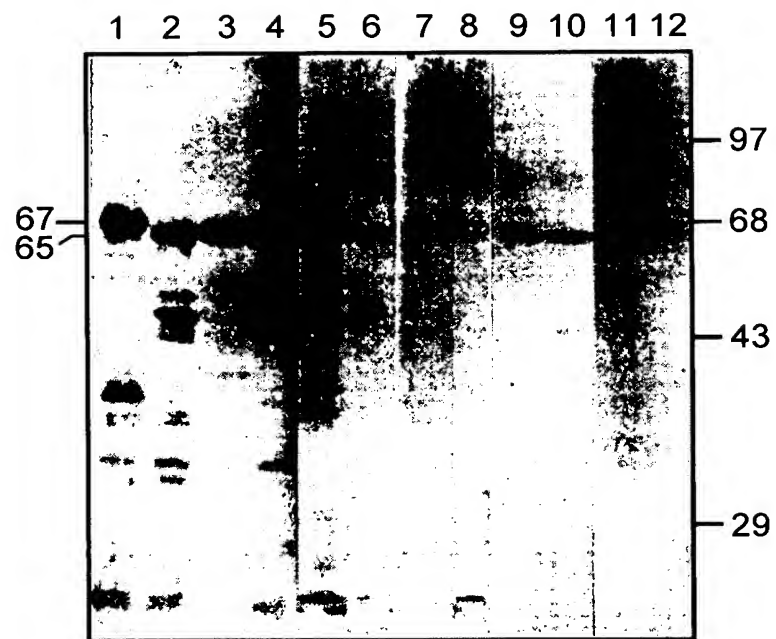


Figure 7